

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10 | 648825A
Source: IFW16
Date Processed by STIC: 5/24/15

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 05/24/2005

PATENT APPLICATION: US/10/648,825A

TIME: 08:56:09

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05242005\J648825A.raw

3 <110> APPLICANT: Ni, Jian
 4 Gentz, Reiner L
 5 Yu, Guo-Liang
 6 Su, Jeffrey
 7 Rosen, Craig A
 9 <120> TITLE OF INVENTION: Death Domain Containing Receptor 5
 11 <130> FILE REFERENCE: 1488.131000C
 13 <140> CURRENT APPLICATION NUMBER: 10/648,825A
 14 <141> CURRENT FILING DATE: 2003-08-27
 16 <150> PRIOR APPLICATION NUMBER: 60/040,846
 17 <151> PRIOR FILING DATE: 1997-03-17
 19 <150> PRIOR APPLICATION NUMBER: 60/054,021
 20 <151> PRIOR FILING DATE: 1997-07-29
 22 <150> PRIOR APPLICATION NUMBER: 09/042,538
 23 <151> PRIOR FILING DATE: 1998-03-17
 25 <150> PRIOR APPLICATION NUMBER: 60/132,498
 26 <151> PRIOR FILING DATE: 1998-05-04
 28 <150> PRIOR APPLICATION NUMBER: 60/133,238
 29 <151> PRIOR FILING DATE: 1998-05-07
 31 <150> PRIOR APPLICATION NUMBER: 60/148,939
 32 <151> PRIOR FILING DATE: 1998-08-13
 34 <150> PRIOR APPLICATION NUMBER: 09/565,009
 35 <151> PRIOR FILING DATE: 2000-05-04
 37 <150> PRIOR APPLICATION NUMBER: 60/406,307
 38 <151> PRIOR FILING DATE: 2002-08-28
 40 <150> PRIOR APPLICATION NUMBER: 60/413,747
 41 <151> PRIOR FILING DATE: 2002-09-27
 43 <160> NUMBER OF SEQ ID NOS: 14
 45 <170> SOFTWARE: PatentIn version 3.1
 47 <210> SEQ ID NO: 1
 48 <211> LENGTH: 1600
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Homo sapiens
 53 <220> FEATURE:
 54 <221> NAME/KEY: CDS
 55 <222> LOCATION: (130)..(1362)
 57 <220> FEATURE:
 58 <221> NAME/KEY: sig_peptide
 59 <222> LOCATION: (130)..(282)
 61 <220> FEATURE:
 62 <221> NAME/KEY: mat_peptide
 63 <222> LOCATION: (283)..(1362)
 65 <400> SEQUENCE: 1

P.6

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66 cacgcgtccg cgggcgcggc cggagaaccc cgcaatcttt gcgcccacaa aatacaccga      60
68 cgatgcccga tctacttttaa gggctgaaac ccacgggcct gagagactat aagagcgttc      120
70 cctaccgcc atg gaa caa cgg gga cag aac gcc ccg gcc gct tcg ggg gcc      171
71      Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala
72      -50      -45      -40
74 cgg aaa agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct      219
75 Arg Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
76      -35      -30      -25
78 ggg ccc cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg      267
79 Gly Pro Arg Val Pro Lys Thr Leu Val Leu Val Ala Ala Val Leu
80      -20      -15      -10
82 ctg ttg gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct      315
83 Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala
84 -5      -1 1      5      10
86 ccc cag cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag      363
87 Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu
88      15      20      25
90 gga ttg tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc      411
91 Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys
92      30      35      40
94 atc tcc tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc      459
95 Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu
96      45      50      55
98 ctt ttc tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta      507
99 Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu
100 60      65      70      75
102 agt ccc tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc      555
103 Ser Pro Cys Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly
104      80      85      90
106 acc ttc cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca      603
107 Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
108      95      100      105
110 ggg tgt ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt      651
111 Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser
112      110      115      120
114 gac atc gaa tgt gtc cac aaa gaa tca ggc atc atc ata gga gtc aca      699
115 Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr
116      125      130      135
118 gtt gca gcc gta gtc ttg att gtg gct gtg ttt gtt tgc aag tct tta      747
119 Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu
120 140      145      150      155
122 ctg tgg aag aaa gtc ctt cct tac ctg aaa ggc atc tgc tca ggt ggt      795
123 Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly
124      160      165      170
126 ggt ggg gac cct gag cgt gtg gac aga agc tca caa cga cct ggg gct      843
127 Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala
128      175      180      185
130 gag gac aat gtc ctc aat gag atc gtg agt atc ttg cag ccc acc cag      891
131 Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln

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132          190          195          200
134 gtc cct gag cag gaa atg gaa gtc cag gag cca gca gag cca aca ggt      939
135 Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
136          205          210          215
138 gtc aac atg ttg tcc ccc ggg gag tca gag cat ctg ctg gaa ccg gca      987
139 Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala
140 220          225          230          235
142 gaa gct gaa agg tct cag agg agg agg ctg ctg gtt cca gca aat gaa      1035
143 Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu
144          240          245          250
146 ggt gat ccc act gag act ctg aga cag tgc ttc gat gac ttt gca gac      1083
147 Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp
148          255          260          265
150 ttg gtg ccc ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc      1131
151 Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu
152          270          275          280
154 atg gac aat gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg      1179
155 Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg
156          285          290          295
158 gac acc ttg tac acg atg ctg ata aag tgg gtc aac aaa acc ggg cga      1227
159 Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
160 300          305          310          315
162 gat gcc tct gtc cac acc ctg ctg gat gcc ttg gag acg ctg gga gag      1275
163 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu
164          320          325          330
166 aga ctt gcc aag cag aag att gag gac cac ttg ttg agc tct gga aag      1323
167 Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys
168          335          340          345
170 ttc atg tat cta gaa ggt aat gca gac tct gcc atg tcc taagtgtgat      1372
171 Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
172          350          355          360
174 tctcttcagg aagtgagacc ttccctggtt tacctttttt ctggaaaaag cccaactgga      1432
176 ctccagtcag taggaaagtg ccacaattgt cacatgaccg gtactggaag aaactctccc      1492
178 atccaacatc acccagtgga tggaacatcc tgtaactttt cactgcactt ggcattattt      1552
180 ttataagctg aatgtgataa taaggacact atggaaaaaa aaaaaaaaaa      1600
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 411
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens
188 <400> SEQUENCE: 2
190 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
191 -50          -45          -40
194 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
195 -35          -30          -25          -20
198 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Val Leu Leu Leu
199          -15          -10          -5
202 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
203 -1 1          5          10
206 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu

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207      15                      20                      25
210 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
211 30                      35                      40                      45
214 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
215                      50                      55                      60
218 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
219                      65                      70                      75
222 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
223                      80                      85                      90
226 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
227                      95                      100                      105
230 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
231 110                      115                      120                      125
234 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
235                      130                      135                      140
238 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
239                      145                      150                      155
242 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
243                      160                      165                      170
246 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
247                      175                      180                      185
250 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
251 190                      195                      200                      205
254 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
255                      210                      215                      220
258 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
259                      225                      230                      235
262 Glu Arg Ser Gln Arg Arg Arg Leu Val Pro Ala Asn Glu Gly Asp
263                      240                      245                      250
266 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
267                      255                      260                      265
270 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
271 270                      275                      280                      285
274 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
275                      290                      295                      300
278 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
279                      305                      310                      315
282 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
283                      320                      325                      330
286 Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
287                      335                      340                      345
290 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
291 350                      355                      360
297 <210> SEQ ID NO: 3
298 <211> LENGTH: 455
299 <212> TYPE: PRT
300 <213> ORGANISM: human
302 <400> SEQUENCE: 3
304 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu

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305 1          5          10          15
307 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
308          20          25          30
310 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
311          35          40          45
313 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
314          50          55          60
316 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
317 65          70          75          80
319 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
320          85          90          95
322 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
323          100         105         110
325 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
326          115         120         125
328 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
329          130         135         140
331 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
332 145          150         155         160
334 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
335          165         170         175
337 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
338          180         185         190
340 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
341          195         200         205
344 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
345          210         215         220
347 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
348 225          230         235         240
350 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
351          245         250         255
353 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
354          260         265         270
356 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
357          275         280         285
359 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
360          290         295         300
362 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
363 305          310         315         320
365 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
366          325         330         335
368 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
369          340         345         350
371 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
372          355         360         365
374 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
375          370         375         380
377 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
378 385          390         395         400

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/24/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 152,199,272,285,310,322,329,331,344,353,363,368,370,374,376

Seq#:6; N Pos. 388,393,403,407,409,410,414,416,421,424,426,451,452,462,463

Seq#:6; N Pos. 466,468,469,471,486,489,495,497,502,503,504

Seq#:14; N Pos. 37,79,81,124,233

VERIFICATION SUMMARY

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L:740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:120

M:341 Repeated in SeqNo=6

L:879 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0

M:341 Repeated in SeqNo=14